

#5

## RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/501,844  
Source: PLT/10  
Date Processed by STIC: 9/6/05

***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 09/06/2005

PATENT APPLICATION: US/10/501,814

TIME: 11:28:50

Input Set : A:\US10501814-seq.list.txt

Output Set: N:\CRF4\09062005\J501814.raw

3 <110> APPLICANT: Evotec NeuroSciences GmbH  
 5 <120> TITLE OF INVENTION: Diagnostic and therapeutic use of a voltage-gated ion  
 6 channel for neurodegenerative diseases  
 8 <130> FILE REFERENCE: P67564US1  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/501,814  
 C--> 11 <141> CURRENT FILING DATE: 2004-07-19  
 13 <160> NUMBER OF SEQ ID NOS: 15  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 272  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA fragment  
 24 of the human SCN2A gene  
 26 <400> SEQUENCE: 1  
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 28 taatgacatg aagaatgagg tottggtaga acaatttgct tcactttacc actgatatat 120  
 29 ggcttccat attagacttc tgaacagggg aaggaataag atacagcagc ataggcaaga 180  
 30 taaacatgca gcagtgcacg cttcaaacta taatggaacc aattacatca tattacctgt 240  
 31 tggaaagcttg caaactatac ttactggggt ac 272  
 34 <210> SEQ ID NO: 2  
 35 <211> LENGTH: 8292  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Artificial Sequence  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: Description of Artificial Sequence: cDNA of the  
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 43 <400> SEQUENCE: 2  
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 46 gctattgaac aacgcattgc agaagagaaa gctaagagac ccaaacagga acgcaaggat 180  
 47 gaggatgatg aaaatggccc aaagccaaac agtgacttgg aagcaggaaa atctcttcca 240  
 48 ttttattatg gagacattcc tccagagatg gtgtcagtgc ccctggagga tctggacccc 300  
 49 tactatatca ataagaaaac gtttatagta ttgataaaag ggaaagcaat ctctcgattc 360  
 50 agtgcaccc ctgcccctta catttttaact cccttcaacc ctattagaaa attagctatt 420  
 51 aagattttgg tacattctt attcaatatg ctcattatgt gcacgattct taccaactgt 480  
 52 gtatttatga ccatgagtaa ccctccagac tggacaaaga atgtggagta tacctttaca 540  
 53 ggaatttata ctttgaatc attattaaa atacttgcaa ggggctttg tttagaagat 600  
 54 ttcacatttt tacgggatcc atggaattgg ttggattca cagtcattac ttttgcata 660  
 55 gtgacagagt ttgtggacct gggcaatgtc tcagcgttga gaacattcag agttctccga 720  
 56 gcattgaaaa caatttcagt cattccaggc ctgaagacca ttgtgggggc cctgatccag 780  
 57 tcagtgaaga agctttctga tgtcatgatc ttgactgtgt tctgtctaag cgtgtttgcg 840

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107 tatgctgaca aggtttcac ttacatattc attctggaaa tgctgctaaa gtgggttgca 3840  
 108 tatggtttc aagtgtattt taccaatgcc tggtgctggc tagacttcct gattgttgat 3900  
 109 gtctcaactgg ttagcttaac tgcaaattgcc ttgggttact cagaacttgg tgccatcaaa 3960  
 110 tccctcagaa cactaagagc tctgaggcca ctgagagctt tgcccgtt tgaaggaatg 4020  
 111 agggttgtt taaatgtct ttttaggagcc attccatcta tcataatgtt acttctgtt 4080  
 112 tgtctgatct tttggctaatttccatctc atggaggtga atctcttgc tggcaagttt 4140  
 113 taccattgtt ttaatttacac cactggagag atgtttgtt gtaagcgtt caacaactac 4200  
 114 agtgagtgca aagctctcat tgagagcaat caaactgcca ggtggaaaaaa tggaaaggtt 4260  
 115 aactttgata acgttagact tggatatctg tctctacttc aagtagccac gtttaaggga 4320  
 116 tggatggata ttatgttatgc agctgttgc tcaacaaatg tagaattaca accaagtat 4380  
 117 gaagacaacc tgcataatgtt tcttttattt gtcataatca ttattttttgg ttcattctt 4440  
 118 accttgaatc ttttcatatgg tgcataatca gataacttca accaacaagaa aaagaagttt 4500  
 119 ggaggtcaag acattttat gacagaagaa cagaagaaat actacaatgc aatgaaaaaaa 4560  
 120 ctgggttcaa agaaaccaca aaaacccata cctcgacctg ctaacaaattt ccaaggaatg 4620  
 121 gtcatttgcattt ttgttacccaa acaagtctt gataatcagca tcataatgtt catctgcctt 4680  
 122 aacatggtca ccatgtatggt ggaaaccatg gaccagatc aagaaatgac aaacattctg 4740  
 123 tactggatta atctgttgc tattgttgc ttcactggag aatgtgttgc gaaactgatc 4800  
 124 tctcttcgtt actactattt cactatttggat tggaaatattt ttgattttgtt ggtggcattt 4860  
 125 ctctccattt taggaatgtt tctggctgaa ctgatagaaa agtattttgtt gtcccctacc 4920  
 126 ctgttccgag tgatccgtt tgcaggattt ggccaaatcc tacgwctgtt caaaggagca 4980  
 127 aaggggatcc gcacgctgtt ctggcttgc atgatgtccc ttccctgcgtt gtttaacatc 5040  
 128 ggccttcattt ttttcatatggt catgttcatc tacggcatct ttggatgttcaatcc 5100  
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 130 atgatctgcc tggatccaaat tacaacatctt gctggctggg atggattgtt agcacctatt 5220  
 131 cttaatatgtt gacccatccaa ctgtgaccctt gacaaatgtt accctggaaatc ctcagttaaa 5280  
 132 ggagactgtt ggaaccatccatc tggatggattt ttcttttttgc tcaatgttcatc catcatatcc 5340  
 133 ttccctggat tggatccatgtt gatcgatccatc tgcataatccatc agaacttcag tggatgttgc 5400  
 134 gaagaaatgtt gatcgatccatc tggatggattt gactttgaga tggatgttgc gtttggggag 5460  
 135 aagtttgcattt cccatgttgcac ccgtttata gatgttgcac aacttttgcattt ttttgcagat 5520  
 136 ggcctggatcc tcccttcattt catagccaaatccaaatccatc tccagctcat tgcacatggat 5580  
 137 ctgcatttgcattt tggatggatccatc tgcataatccatc tgcataatccatc tcttatttgc ttttacaaatcc 5640  
 138 cgtgttttttgcattt gatgttgcattt gatgttgcac tacagatggatccatc agagcgatcc 5700  
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 140 caagaggaggatccatc tggatggatccatc tggatggatccatc gacgcttacatc ttttacaaatcc 5820  
 141 aaagtttacccaaatccatc tggatggatccatc tggatggatccatc gacgcttacatc ttttacaaatcc 5880  
 142 cccatccatc tggatggatccatc tggatggatccatc tggatggatccatc attcaactcc agagaaaacc 5940  
 143 gatgttgcattt tggatggatccatc tggatggatccatc tggatggatccatc gatgttgcac accagaaaaaa 6000  
 144 gaaaaatggatccatc tggatggatccatc tggatggatccatc gatgttgcac gggaaatgttgc 6060  
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 147 acaaatgttcatc tggatggatccatc tggatggatccatc tggatggatccatc gatgttgcac gggaaatgttgc 6240  
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 149 cactgctgaaatccatc tggatggatccatc tggatggatccatc tggatggatccatc gatgttgcac gggaaatgttgc 6360  
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 154 tataacttgcattt tggatggatccatc tggatggatccatc tggatggatccatc gatgttgcac gggaaatgttgc 6660  
 155 cactatccatc tggatggatccatc tggatggatccatc tggatggatccatc gatgttgcac gggaaatgttgc 6720

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156 cttaaatagc tattcgattt tttaagggtgt ctcatccaga aaaaatttaa tggcctgt 6780  
 157 aatgttccat agaatcaca gattaaaga gttgtttat tttacataa cccattaaat 6840  
 158 gtacatgtat atatgtat atgtatatgt gcgtgtat acatataat gtatacacac 6900  
 159 atgcacacac agagatatac acataccatt acattgtcat tcacagttcc agcagcatga 6960  
 160 ctatcacatt tttgataagt gtccttggc ataaaataaa aatatcctat cagtccttc 7020  
 161 taagaaggct gaattgacca aaaaacatcc ccaccaccac tttataaagt tgattctgct 7080  
 162 ttatcctgca gtattgtta gccatctt gctcttggta aggttgacat agtataatgtc 7140  
 163 aatttaaaaa ataaaagtct gctttgtaaa tagtaattt acccagtggt gcatgtttga 7200  
 164 gcaaacaaaa atgatgattt aagcacacta cttattgcat caaatatgtt ccacagtaag 7260  
 165 tatagtttgc aagcttcaa caggtaatat gatgtattt gttccattt agttgaagc 7320  
 166 tgtcactgct gcatgtttat cttgcctatg ctgtgttac ttattccttc cactgttcag 7380  
 167 aagtctaata tggaaagcca tatatcagt gtaaagtgaa gcaaattgtt ctaccaagac 7440  
 168 ctcattcttc atgtcattaa gcaatagggt gcagcaaca aggaagagct tcttgcttt 7500  
 169 tattcttcca accttaattt aacactcaat gatgttttcc ggtttttttt aacatgttg 7560  
 170 caagctgtttt aaatctgtttt aaaaatataat gtttaggttt tctaagaaaa tataaataact 7620  
 171 gtaaaaaagt catttttattt tatttttcag cctttgtac gtaaaatgag aaattaaaag 7680  
 172 tatcttcagg tggatgtcac agtcaactt gtttagtttct gttccttagca cttttaaattt 7740  
 173 gaagcacttc acaaaaataag aagcaaggac taggatgcag tggatgttc tgctttttt 7800  
 174 ttagtactgt aaacttgcac acatttcaat gtgaaacaaa tctcaaactg agtcaatgt 7860  
 175 ttatttgcattt tcaatagtaa tgccttataca ttgaaagagg cttaaagaaaa aaaaaaatca 7920  
 176 gctgataactc ttggcattgc ttgaatccaa tggatccacc tagtctttt atttagtaat 7980  
 177 catcagtctt ttccaatgtt tggatccaca gatagatctt attgaccat atggcaactag 8040  
 178 aactgtatca gatataatat gggatcccag cttttttcc tctcccacaa aaccaggtag 8100  
 179 tgaagttata ttaccagttt cagcaaaaata ctttgggttt cacaagcaac aataaatagt 8160  
 180 gattctttat actgaagcta ttgacttgc gttgttttgc gaaatgcattt cagaaaaatgt 8220  
 181 ctgttaccat aaagaacggt aaaccacattt acaatcaagc caaaagaata aaggttcgc 8280  
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 185 <210> SEQ ID NO: 3  
 186 <211> LENGTH: 2005  
 187 <212> TYPE: PRT  
 188 <213> ORGANISM: Homo sapiens  
 189 <400> SEQUENCE: 3  
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 191 1 5 10 15  
 192 Phe Thr Arg Glu Ser Leu Ala Ala Ile Glu Gln Arg Ile Ala Glu Glu  
 193 20 25 30  
 194 Lys Ala Lys Arg Pro Lys Gln Glu Arg Lys Asp Glu Asp Asp Glu Asn  
 195 35 40 45  
 196 Gly Pro Lys Pro Asn Ser Asp Leu Glu Ala Gly Lys Ser Leu Pro Phe  
 197 50 55 60  
 198 Ile Tyr Gly Asp Ile Pro Pro Glu Met Val Ser Val Pro Leu Glu Asp  
 199 65 70 75 80  
 200 Leu Asp Pro Tyr Tyr Ile Asn Lys Lys Thr Phe Ile Val Leu Asn Lys  
 201 85 90 95  
 202 Gly Lys Ala Ile Ser Arg Phe Ser Ala Thr Pro Ala Leu Tyr Ile Leu  
 203 100 105 110  
 204 Thr Pro Phe Asn Pro Ile Arg Lys Leu Ala Ile Lys Ile Leu Val His  
 205 115 120 125  
 206 Ser Leu Phe Asn Met Leu Ile Met Cys Thr Ile Leu Thr Asn Cys Val

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216 130 135 140  
 218 Phe Met Thr Met Ser Asn Pro Pro Asp Trp Thr Lys Asn Val Glu Tyr  
 219 145 150 155 160  
 221 Thr Phe Thr Gly Ile Tyr Thr Phe Glu Ser Leu Ile Lys Ile Leu Ala  
 222 165 170 175  
 224 Arg Gly Phe Cys Leu Glu Asp Phe Thr Phe Leu Arg Asp Pro Trp Asn  
 225 180 185 190  
 227 Trp Leu Asp Phe Thr Val Ile Thr Phe Ala Tyr Val Thr Glu Phe Val  
 228 195 200 205  
 230 Asp Leu Gly Asn Val Ser Ala Leu Arg Thr Phe Arg Val Leu Arg Ala  
 231 210 215 220  
 233 Leu Lys Thr Ile Ser Val Ile Pro Gly Leu Lys Thr Ile Val Gly Ala  
 234 225 230 235 240  
 236 Leu Ile Gln Ser Val Lys Lys Leu Ser Asp Val Met Ile Leu Thr Val  
 237 245 250 255  
 239 Phe Cys Leu Ser Val Phe Ala Leu Ile Gly Leu Gln Leu Phe Met Gly  
 240 260 265 270  
 242 Asn Leu Arg Asn Lys Cys Leu Gln Trp Pro Pro Asp Asn Ser Ser Phe  
 243 275 280 285  
 245 Glu Ile Asn Ile Thr Ser Phe Phe Asn Asn Ser Leu Asp Gly Asn Gly  
 246 290 295 300  
 248 Thr Thr Phe Asn Arg Thr Val Ser Ile Phe Asn Trp Asp Glu Tyr Ile  
 249 305 310 315 320  
 251 Glu Asp Lys Ser His Phe Tyr Phe Leu Glu Gly Gln Asn Asp Ala Leu  
 252 325 330 335  
 254 Leu Cys Gly Asn Ser Ser Asp Ala Gly Gln Cys Pro Glu Gly Tyr Ile  
 255 340 345 350  
 257 Cys Val Lys Ala Gly Arg Asn Pro Asn Tyr Gly Tyr Thr Ser Phe Asp  
 258 355 360 365  
 260 Thr Phe Ser Trp Ala Phe Leu Ser Leu Phe Arg Leu Met Thr Gln Asp  
 261 370 375 380  
 263 Phe Trp Glu Asn Leu Tyr Gln Leu Thr Leu Arg Ala Ala Gly Lys Thr  
 264 385 390 395 400  
 266 Tyr Met Ile Phe Phe Val Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu  
 267 405 410 415  
 269 Ile Asn Leu Ile Leu Ala Val Val Ala Met Ala Tyr Glu Glu Gln Asn  
 270 420 425 430  
 272 Gln Ala Thr Leu Glu Glu Ala Glu Gln Lys Glu Ala Glu Phe Gln Gln  
 273 435 440 445  
 275 Met Leu Glu Gln Leu Lys Lys Gln Gln Glu Ala Gln Ala Ala Ala  
 276 450 455 460  
 278 Ala Ala Ala Ser Ala Glu Ser Arg Asp Phe Ser Gly Ala Gly Gly Ile  
 279 465 470 475 480  
 281 Gly Val Phe Ser Glu Ser Ser Ser Val Ala Ser Lys Leu Ser Ser Lys  
 282 485 490 495  
 284 Ser Glu Lys Glu Leu Lys Asn Arg Arg Lys Lys Lys Lys Gln Lys Glu  
 285 500 505 510  
 287 Gln Ser Gly Glu Glu Lys Asn Asp Arg Val Leu Lys Ser Glu Ser  
 288 515 520 525

**VERIFICATION SUMMARY**

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TIME: 11:28:51

Input Set : A:\US10501814-seq list.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date